

SEQUENCE LISTING

<110> Sumitomo Chemical Co., Ltd

5

<120> PROCESS FOR PRODUCING OPTICALLY ACTIVE 4-HALO-3-HYDROXYBUTANOATE

<130>

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<140>

<141>

<160> 27

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<170> PatentIn Ver. 2.1

<210> 1

<211> 325

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<212> PRT

<213> Penicillium citrinum

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Tyr	Thr	Ala	Val	Thr	Thr	Ala	Leu	Lys	Thr	Gly	Tyr	Arg	His	Leu	Asp
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Cys	Ala	Trp	Tyr	Tyr	Leu	Asn	Glu	Gly	Glu	Val	Gly	Glu	Ile	Arg
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Asp	Phe	Leu	Lys	Glu	Asn	Pro	Ser	Val	Lys	Arg	Glu	Asp	Ile	Phe	Val
65													80		

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Cys	Thr	Lys	Val	Trp	Asn	His	Leu	His	Arg	Tyr	Glu	Asp	Val	Leu	Trp
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85

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Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met
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 Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu
 5 115 120 125
 Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr
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 10 Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp
 145 150 155 160
 Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu
 165 170 175
 15 Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile
 180 185 190
 Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe
 20 195 200 205
 Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn
 210 215 220
 Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn
 25 225 230 235 240
 Glu Ile Ala Glu Lys Gly Asn Thr Leu Ala Gln Val Leu Ile Ala
 245 250 255
 30 Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro
 260 265 270
 Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp
 35 275 280 285
 Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val
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Lys Asn Leu Ser Ala
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<222> (1)..(978)

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20 ggc gtc ggc ttt ggt acc ttc gct agt gaa ggt tcc aag ggc gag acc 96
Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr
20 25 30

25 tat act gct gtc acc act gcc ctg aag acc ggt tac cgt cac ttg gac 144
Tyr Thr Ala Val Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp
35 35 40 45

30 tgg gcc tgg tac tac ctg aac gag ggt gag gtt ggt gag ggt atc cgt 192
Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Ile Arg
50 55 60

35 gac ttc ctg aag gag aac ccc tgg gtc aag cgt gag gac atc ttc gtc 240
Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val
65 70 75 80

40 tgc acc aag gtc tgg aac cac ctc cac cgt tat gag gac gtc ctc tgg 288
Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp
85 90 95

45 tcc att gac gac tcc ctg aag cgt ctt gga ctt gac tac gtt gat atg 336
Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met
100 105 110

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	Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu	
	115 120 125	
5	ccc aag att ggc cct gac ggc aaa tac gtc att ctc aag gac ctg acc	432
	Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr	
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10	gag aac ccc gag ccc aca tgg cgc gct atg gag aag att tat gag gat	480
	Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp	
	145 150 155 160	
15	cgc aag gcc agg tcc att ggt gtc tcc aac tgg acc att gcc gac ctt	528
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20	gag att cac ccc ttc ctg ccc aac gag gag ctg gtg cag tac tgc ttc	624
	Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe	
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25	tcc aag aac att atg ccc gtg gcc tac tct cct ctg ggc tcg cag aac	672
	Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn	
	210 215 220	
30	cag gtt ccc acc acc ggt gag cgg gtc agc gag aac aag act ctg aac	720
	Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn	
	225 230 235 240	
35	gag atc gcc gag aag ggc ggc aac acc ctt gct cag gtt ctt att gcc	768
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40	tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc	816
	Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro	
	260 265 270	
	aag cgc att gag tcc aac ttc aag agc att gag ctc tcc gat gcc gac	864
	Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp	

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	Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val			
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	<213> Penicillium citrinum			
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Lys

10 <210> 6
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<212> PRT
<213> *Penicillium citrinum*

15 <400> 6
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1 5 10

20 <210> 7
<211> 14
<212> PRT
<213> *Penicillium citrinum*

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30 <210> 8
<211> 20
<212> DNA
<213> Artificial Sequence

35 <220>
<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

40 <400> 8 20
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<210> 9

<211> 20

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<213> Artificial Sequence

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<223> Description of Artificial Sequence:Designed
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<210> 10

15 <211> 20

<212> DNA

<213> Artificial Sequence

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20 <223> Description of Artificial Sequence:Designed
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tangcnacng gcataatgtt

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30 <213> Artificial Sequence

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<223> Description of Artificial Sequence:Designed
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<211> 20

<212> DNA

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<223> Description of Artificial Sequence:Designed
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<210> 13

<211> 20

<212> DNA

<213> Artificial Sequence

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<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

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<210> 14

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<212> DNA

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<220>

<223> Description of Artificial Sequence:Designed
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tangcnacng goattatgtt

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<210> 15

<211> 697

<212> DNA

<213> Escherichia coli

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 agtgaaggtt ccaagggcga aacctatnct gctgtacca ctgcctgaa aaccggttac 180
 cgtcncttgg actgtgcctg gtactacctg aacaagggtg aggttggtga gggtnccgt 240
 gacttcctga aggaaaaccc ctccgtgaag cgtgaggaca tcttcgtctg caccagggtg 300
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 ggccagggtg agccaaaaat tggccctgac ggcaaatacn tcnttcctaa ggacctgacc 480
 gaaanccna ncccacctgg cgcgtatgg aaaaaatttn tgangatccc aaggccagg 540
 10 ccattggtgt ttccaaatgg accattggcg accttgagaa gatgtccaag ttngccaagg 600
 tnatgcctca cgccaaaccag atcgagatcc accccttcct gcccaacogag gagctggtgc 660
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15 <210> 16
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 <213> Artificial Sequence

20 <220>
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25 <400> 16
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30 <210> 17
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 <213> Artificial Sequence

35 <220>
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 oligonucleotide primer for PCR

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 caaccagatc gagattcacc 20

<210> 18
 <211> 331

<212> DNA

<213> Escherichia coli

<400> 18

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 gcccgtgaaga ccgggttaccg tcacttggac tgtgcctgggt actacctgaa cgagggtgag 240
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 10 ttcgtctgca ccaagggtgtg gaaccacac 331

<210> 19

<211> 743

<212> DNA

<213> Escherichia coli

<400> 19

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 cggtgagcgg gtcagcgaga acaagactct gaacgagatc gcccggaaagg gcccggaaac 180
 ctttgctcg gtttttattt cctgggtct gcccgtggc tacgtcgttc tcccaagag 240
 ctccaaaccc aagcgcattt agtccaactt caagagcatt gagctctccg atgcccactt 300
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 25 tttcgatat gatgttgcgc cggaggagac cggcaagaac ctgtctcggt gaatctctac 420
 gaaattataa aatnacaccn acnnaaaanc aagcgaaag gatgatnccc aaaantttt 480
 agggtttctt ggttggaaac gtttattttt cccgaantga angaatagat gancntgatt 540
 tctccaaaaa aaaaaaaaaa aaaaacggtc cggccgcgtt ccnnnggggg gcccgggtcc 600
 caattnccn cttatnattt aattttttt taanggggncc aaattccncc nnatttcont 660
 30 cnanatttgn nggccgcctc caaactttcn tcntnaaagg gncccaattc ccccccnatt 720
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<210> 20

<211> 21

<212> DNA

<213> Artificial Sequence

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40 <223> Description of Artificial Sequence: Designed
originucleotide primer for PCR

27

gccatggcta tgtcttaacgg aaagact

<210> 24

5 <211> 29

<212> DNA

<213> Artificial Sequence

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10 <223> Description of Artificial Sequence: Designed
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15 cggatccgtt ataattttagt agagattca

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<210> 25

<211> 21

<212> DNA

20 <213> Artificial Sequence

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<223> Description of Artificial Sequence: Designed
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gatcatcata gcaggaggatca t

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30 <210> 26

<211> 21

<212> DNA

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35 <220>

<223> Description of Artificial Sequence: Designed
oligonucleotide primer for PCR

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<210> 27
 <211> 786
 <212> DNA
 <213> Escherichia coli

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<220>
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 <222> (1)..(786)

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15 acc ggt tta gga aaa gca atg gcg att cgt ttt gcg aca gaa aaa gct 96
 Thr Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Ala Thr Glu Lys Ala
 20 25 30

20 aaa gta gtt gtg aac tat cgt tcg aaa gaa gaa gct aac agc gtt 144
 Lys Val Val Val Asn Tyr Arg Ser Lys Glu Glu Glu Ala Asn Ser Val
 35 40 45

25 tta gaa gaa att aaa aaa gtg ggc gga gag gct att gcc gtc aaa ggt 192
 Leu Glu Glu Ile Lys Lys Val Gly Gly Glu Ala Ile Ala Val Lys Gly
 50 55 60

30 gat gta aca gtt gag tct gat gtg atc aat tta gtt caa tct gct att 240
 Asp Val Thr Val Glu Ser Asp Val Ile Asn Leu Val Gln Ser Ala Ile
 65 70 75 80

35 aaa gaa ttt gga aag cta gac gtt atg att aat aac gca gga atg gaa 288
 Lys Glu Phe Gly Lys Leu Asp Val Met Ile Asn Asn Ala Gly Met Glu
 85 90 95

40 aat ccg gtt tcg tct cat gaa atg tct tta agt gat tgg aat aaa gtc 336
 Asn Pro Val Ser Ser His Glu Met Ser Leu Ser Asp Trp Asn Lys Val
 100 105 110

45 att gat acg aac tta acg gga gca ttt tta ggc agc cgt gaa gcg att 384
 Ile Asp Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
 115 120 125

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ccaagggtgtg gaaccacaccc c

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5 <210> 21

<211> 21

<212> DNA

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<223> Description of Artificial Sequence: Designed
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<211> 417

<212> DNA

<213> Escherichia coli

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agaagaatgg ccagggtgag cccaaaggattg gccctgacgg caaatacgcc attctcaagg 180
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tcgccaagggt catgcctcac gccaaccaga tcgagattca ccccttcctg cccaaacgagg 360
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35 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Designed
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 130 135 140

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 Ser Val His Glu Lys Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
 145 150 155 160

10 agt aaa ggc gga atg aag ctc atg acc gaa aca ctt gca tta gaa tac 528
 Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
 165 170 175

15 gct cca aaa ggt att cgt gta aat aac att gga ccg gga gcg att aat 576
 Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
 180 185 190

20 aca ccg att aac gct gag aaa ttt gct gat cct gag cag cgt gca gat 624
 Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp
 195 200 205

25 gta gaa agc atg att cca atg gga tac att gga gag ccg gaa gaa att 672
 Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile
 210 215 220

30 gca gcg gtt gct gca tgg cta gct tct tca gag gca agt tat gta aca 720
 Ala Ala Val Ala Ala Trp Leu Ala Ser Ser Glu Ala Ser Tyr Val Thr
 225 230 235 240

35 ggg att aca ctc ttt gct gac ggc ggt atg aca cag tac cca tca ttc 768
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<211> 996

40 <212> DNA

<213> Penicillium citrinum

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<222> (1)..(978)

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	1	5							10						15		
10	ggc	gtc	ggc	ttt	ggt	acc	ttc	gct	agt	gaa	ggt	tcc	aag	ggc	gag	acc	96
	Gly	Val	Gly	Phe	Gly	Thr	Phe	Ala	Ser	Glu	Gly	Ser	Lys	Gly	Glu	Thr	
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15	tat	act	gct	gtc	acc	act	gcc	ctg	aag	acc	ggt	tac	cgt	cac	ttg	gac	144
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25	gac	ttc	ctg	aag	gag	aac	ccc	tcg	gtg	aag	cgt	gag	gac	atc	ttc	gtc	240
	Asp	Phe	Leu	Lys	Glu	Asn	Pro	Ser	Val	Lys	Arg	Glu	Asp	Ile	Phe	Val	
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30	tgc	acc	aag	gtg	tgg	aac	cac	ctc	cac	cgt	tat	gag	gac	gtc	ctc	tgg	288
	Cys	Thr	Lys	Val	Trp	Asn	His	Leu	His	Arg	Tyr	Glu	Asp	Val	Leu	Trp	
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35	tcc	att	gac	gac	tcc	ctg	aag	cgt	ctt	gga	ctt	gac	tac	gtt	gat	atg	336
	Ser	Ile	Asp	Asp	Ser	Leu	Lys	Arg	Leu	Gly	Leu	Asp	Tyr	Val	Asp	Met	
									100						110		
40	ttc	ctc	gtt	cac	tgg	ccc	att	gct	gco	gag	aag	aat	ggc	cag	ggt	gag	384
	Phe	Leu	Val	His	Trp	Pro	Ile	Ala	Ala	Glu	Lys	Asn	Gly	Gln	Gly	Glu	
									115						125		
45	ccc	aag	att	ggc	cct	gac	ggc	aaa	tac	gtc	att	ctc	aag	gac	ctg	acc	432
	Pro	Lys	Ile	Gly	Pro	Asp	Gly	Lys	Tyr	Val	Ile	Leu	Lys	Asp	Leu	Thr	
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50	gag	aac	ccc	gag	ccc	aca	tgg	cgc	gct	atg	gag	aag	att	tat	gag	gat	480

Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp
145 150 155 160

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Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu
165 170 175

10 gag aag atg tcc aag ttc gcc aag gtc atg cct cac gcc aac cag atc 576
Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile
180 185 190

15 gag att cac ccc ttc ctg ccc aac gag gag ctg gtg cag tac tgc ttc 624
Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe
195 200 205

20 tcc aag aac att atg ccc gtg gcc tac tct cct ctg ggc tcg cag aac 672
Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn
210 215 220

25 cag gtt ccc acc acc ggt gag cgg gtc agc gag aac aag act ctg aac 720
Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn
225 230 235 240

30 gag atc gcc gag aag ggc ggc aac acc ctt gct cag gtt ctt att gcc 768
Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala
245 250 255

35 tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc 816
Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro
260 265 270

40 aag cgc att gag tcc aac ttc aag agc att gag ctc tcc gat gcc gac 864
Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp
275 280 285

45 ttt gaa gcc atc aat gcc gtt gcc aag ggt cgt cac ttc cgt ttc gtc 912
Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val
290 295 300

50 aac atg aag gat act ttc gga tat gat gtc tgg ccc gag gag acc gcc 960
Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala
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aag aac ctg tct gcg tga atctctacga aattataa 996
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5
 <210> 29
 <211> 29
 <212> DNA
 <213> Artificial Sequence

10
 <220>
 <223> Description of Artificial Sequence Designed oligonucleotide primer
 for PCR

15 <400> 29 29
 cggatccgtt cacgcagaca ggttcttgg

20 <210> 30
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25 <220>
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 30 1 5 10 15

ggc gtc ggc ttt ggt acc ttc gct agt gaa ggt tcc aag ggc gag acc 96
 Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr
 20 25 30

35 tat act gct gtc acc act gcc ctg aag acc ggt tac cgt cac ttg gac 144
 Tyr Thr Ala Val Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp
 35 40 45

40 tgt gcc tgg tac tac ctg aac gag ggt gag gtt ggt gag ggt atc cgt 192
 Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg
 50 55 60

gac ttc ctg aag gag aac ccc tcg gtg aag cgt gag gac atc ttc gtc	240
Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val	
65 70 75 80	
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tgc acc aag gtg tgg aac cac ctc cac cgt tat gag gac gtc ctc tgg	288
Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp	
85 90 95	
10 tcc att gac gac tcc ctg aag cgt ctt gga ctt gac tac gtt gat atg	336
Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met	
100 105 110	
15 ttc ctc gtt cac tgg ccc att gct gcc gag aag aat ggc cag ggt gag	384
Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu	
115 120 125	
20 ccc aag att ggc cct gac ggc aaa tac gtc att ctc aag gac ctg acc	432
Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr	
130 135 140	
25 gag aac ccc gag ccc aca tgg cgc gct atg gag aag att tat gag gat	480
Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp	
145 150 155 160	
30 cgc aag gcc agg tcc att ggt gtc tcc aac tgg acc att gcc gac ctt	528
Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu	
165 170 175	
35 gag aag atg tcc aag ttc gcc aag gtc atg cct cac gcc aac cag atc	576
Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile	
180 185 190	
40 gag att cac ccc ttc ctg ccc aac gag gag ctg gtg cag tac tgc ttc	624
Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe	
195 200 205	
tcc aag aac att atg ccc gtg gcc tac tct cct ctg ggc tgc cag aac	672
Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn	
210 215 220	
cag gtt ccc acc acc ggt gag cgg gtc agc gag aac aag act ctg aac	720

225 Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn
 230 235 240

5 gag atc gcc gag aag ggc ggc aac acc ctt gct cag gtt ctt att gcc 768
 Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala
 245 250 255

10 tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc 816
 Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro
 260 265 270

aag cgc att gag tcc aac ttc aag agc att gag ctc tcc gat gcc gac 864
 Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp
 275 280 285

15 ttt gaa gcc atc aat gcc gtt gcc aag ggt cgt cac ttc cgt ttc gtc 912
 Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val
 290 295 300

20 aac atg aag gat act ttc gga tat gat gtc tgg ccc gag gag acc gcc 960
 Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala
 305 310 315 320

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 Lys Asn Leu Ser Ala
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<210> 31

<211> 27

30 <212> DNA

<213> Artificial Sequence

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35 <223> Description of Artificial Sequence Designed oligonucleotide primer
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27

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<210> 32

<211> 23

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<213> Artificial Sequence

<220>

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for PCR

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23

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<210> 33

<211> 28

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence Designed oligonucleotide primer
for PCR

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28

<210> 34

<211> 385

25 <212> PRT

<213> Corynebacterium sp.

<400> 34

Met Lys Ala Ile Gln Tyr Thr Arg Ile Gly Ala Glu Pro Glu Leu Thr

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Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val

20 25 30

35 Thr Ala Ala Gly Val Cys His Ser Asp Asp Phe Ile Met Ser Leu Pro
35 40 45Glu Glu Gln Tyr Thr Tyr Gly Leu Pro Leu Thr Leu Gly His Glu Gly
50 55 60

Ala Gly Lys Val Ala Ala Val Gly Glu Gly Val Glu Gly Leu Asp Ile
 65 70 75 80

5 Gly Thr Asn Val Val Val Tyr Gly Pro Trp Gly Cys Gly Asn Cys Trp
 85 90 95

His Cys Ser Gln Gly Leu Glu Asn Tyr Cys Ser Arg Ala Gln Glu Leu
 100 105 110

10 Gly Ile Asn Pro Pro Gly Leu Gly Ala Pro Gly Ala Leu Ala Glu Phe
 115 120 125

Met Ile Val Asp Ser Pro Arg His Leu Val Pro Ile Gly Asp Leu Asp
 15 130 135 140

Pro Val Lys Thr Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His
 145 150 155 160

20 Ala Ile Lys Arg Ser Leu Pro Lys Leu Arg Gly Gly Ser Tyr Ala Val
 165 170 175

Val Ile Gly Thr Gly Gly Leu Gly His Val Ala Ile Gln Leu Leu Arg
 180 185 190

25 His Leu Ser Ala Ala Thr Val Ile Ala Leu Asp Val Ser Ala Asp Lys
 195 200 205

Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp
 30 210 215 220

Lys Asp Ala Ala Glu Asn Val Arg Lys Ile Thr Gly Ser Gln Gly Ala
 225 230 235 240

35 Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala
 245 250 255

Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly
 40 260 265 270

Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu
 275 280 285

Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu
290 295 300

5 Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Gly Gly Gly Asp
305 310 315 320

Leu Gln Ser Arg Gln Arg Cys Arg Ser Val Ser Thr Thr Gly Cys Arg
325 330 335

10 Asn Ala Gln Arg Pro Cys Gly Cys Gly Pro Trp Ser Val Val Pro Thr
340 345 350

Ala Val Glu Arg Gln Arg Lys Asn Thr Asp Ala Arg Pro Asn Ser Ile
15 355 360 365

Arg Pro Gly Ile Ser Val Arg Asn Ser Val Cys Ala Ser Cys Thr Pro
370 375 380

20 Arg
385

<210> 35
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<220>
30 <221> CDS
<222> (1)..(1158)

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35 Met Lys Ala Ile Gln Tyr Thr Arg Ile Gly Ala Glu Pro Glu Leu Thr
1 5 10 15

gag att ccc aaa ccc gag ccc ggt cca ggt gaa gtg ctc ctg gaa gtc 96
Glu Ile Pro Lys Pro Glu Pro Gly Glu Val Leu Leu Glu Val
40 20 25 30

acc gct gct ggc gtc tgc cac tcg gac gac ttc atc atg agc ctg ccc 144

	Thr Ala Ala Gly Val Cys His Ser Asp Asp Phe Ile Met Ser Leu Pro			
	35	40	45	
5	gaa gag cag tac acc tac ggc ctt ccg ctc acg ctc ggc cac gaa ggc Glu Glu Gln Tyr Thr Tyr Gly Leu Pro Leu Thr Leu Gly His Glu Gly		192	
	50	55	60	
10	gca ggc aag gtc gcc gtc ggc gag ggt gtc gaa ggt ctc gac atc Ala Gly Lys Val Ala Ala Val Gly Glu Gly Val Glu Gly Leu Asp Ile		240	
	65	70	75	80
15	gga acc aat gtc gtc tac ggg cct tgg ggt tgc ggc aac tgt tgg Gly Thr Asn Val Val Tyr Gly Pro Trp Gly Cys Gly Asn Cys Trp		288	
	85	90	95	
20	cac tgc tca caa gga ctc gag aac tat tgc tct ccg gcc caa gaa ctc His Cys Ser Gln Gly Leu Glu Asn Tyr Cys Ser Arg Ala Gln Glu Leu		336	
	100	105	110	
25	gga atc aat cct ccc ggt ctc ggt gca ccc ggc gcg ttg gcc gag ttc Gly Ile Asn Pro Pro Gly Leu Gly Ala Pro Gly Ala Leu Ala Glu Phe		384	
	115	120	125	
30	atg atc gtc gat tct cct ccg cac ctt gtc ccg atc ggt gac ctc gac Met Ile Val Asp Ser Pro Arg His Leu Val Pro Ile Gly Asp Leu Asp		432	
	130	135	140	
35	ccg gtc aag acg gtg ccg ctg acc gac gcc ggt ctg acg ccg tat cac Pro Val Lys Thr Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His		480	
	145	150	155	160
40	gcg atc aag cgt tct ctg ccg aaa ctt ccg gga ggc tcg tac gct gtc gtt Ala Ile Lys Arg Ser Leu Pro Lys Leu Arg Gly Gly Ser Tyr Ala Val		528	
	165	170	175	
	180	185	190	
	cac ctc tog gcg gca acg gtc atc gct ttg gac gtg acg gcg gac aag His Leu Ser Ala Ala Thr Val Ile Ala Leu Asp Val Ser Ala Asp Lys		624	
	195	200	205	

ctc gaa ctg gca acc aag gta ggc gct cac gaa gtc gtt ctg tcc gac	672
Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp	
210 215 220	
5	
aag gac gcg gcc gag aac gtc cgc aag atc act gga agt caa ggc gcc	720
Lys Asp Ala Ala Glu Asn Val Arg Lys Ile Thr Gly Ser Gln Gly Ala	
225 230 235 240	
10 gca ttg gtt ctc gac ttc gtc ggc tac cag ccc acc atc gac acc gcg	768
Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala	
245 250 255	
15 atg gct gtc gcc ggc gtc gga tca gac gtc acg atc gtc ggg atc ggg	816
Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly	
260 265 270	
20 gac ggc cag gcc cac gcc aaa gtc ggg ttc ttc caa agt cct tac gag	864
Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu	
275 280 285	
25 gct tcg gtg aca gtt cog tat tgg ggt gcc cgc aac gag ttg atc gaa	912
Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu	
290 295 300	
30 ttg atc gac ctc gcc cac gcc ggc atc ttc gac atc ggc ggt gga gac	960
Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Gly Gly Asp	
305 310 315 320	
35 ctt cag tct cga caa cgg tgc cga agc gta tcg acg act ggc tgc cgg	1008
Leu Gln Ser Arg Gln Arg Cys Arg Ser Val Ser Thr Thr Gly Cys Arg	
325 330 335	
35 aac gct cag cgg cgg tgc ggt tgt ggt ccc tgg tct gta gta cgg aca	1056
Asn Ala Gln Arg Pro Cys Gly Cys Gly Pro Trp Ser Val Val Pro Thr	
340 345 350	
40 gcg gta gaa cga cag cgg aaa aac act gat gcc cgg cgg aat tcg att	1104
Ala Val Glu Arg Gln Arg Lys Asn Thr Asp Ala Arg Pro Asn Ser Ile	
355 360 365	
45 cgg cgg ggc atc agt gtc aga aat tcg gtc gtc gct agc tgc acg cct	1152

Arg Pro Gly Ile Ser Val Arg Asn Ser Val Cys Ala Ser Cys Thr Pro
370 375 380

cga tga 1158
5 Arg
385